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RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/065,200A**

DATE: 12/09/2002 P.6
TIME: 13:03:56

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF4\12092002\J065200A.raw**

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 3 <110> APPLICANT: Wisnewski, Nancy
 4         Becher, Anna M.
 5         Jarvis, Eric
 7 <120> TITLE OF INVENTION: NOVEL FLEA ECDYSONE AND ULTRASPIRACLE NUCLEIC ACID
MOLECULES, PROTEINS
 8         AND USES THEREOF
10 <130> FILE REFERENCE: FC-4-1
12 <140> CURRENT APPLICATION NUMBER: 10/065,200A
C--> 13 <141> CURRENT FILING DATE: 2002-11-18
15 <150> PRIOR APPLICATION NUMBER: 09/435,019
16 <151> PRIOR FILING DATE: 1999-11-05
18 <150> PRIOR APPLICATION NUMBER: 60/107,559
19 <151> PRIOR FILING DATE: 1998-11-06
21 <160> NUMBER OF SEQ ID NOS: 71
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 446
27 <212> TYPE: DNA
28 <213> ORGANISM: Ctenocephalides felis
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33 cgaaaggaaa agaaggcaca gaaggaaaag gacatcggac caatatcagg taccgttgga    120
35 aaatctgctg ctcccttagc gaattctgca ttacttcaga agcctgatat tttgcctgcg    180
37 gtcatgaaat gcgacccatt acctccagaa gcaactaaag tgaaattttt gtcagacaag    240
39 attcttgctg aaaacagaat tcgaaatgtt ccacctttga ctgcaaatca agaatatgtg    300
41 atcgcaagat tagtgtggta ccaagatgga tatgaacaac cttctgagga agacctacga    360
43 aggataatga taagtacacc aggtgaagat gaagctgttg aatttcggca tataactgaa    420
45 attaccatac ttactgtgca gcttat                                          446
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 446
50 <212> TYPE: DNA
51 <213> ORGANISM: Ctenocephalides felis
53 <400> SEQUENCE: 2
54 ataagctgca cagtaagtat ggtaatttca gttatatgcc gaaattcaac agcttcatct     60
56 tcacctggtg tacttatcat tatccttcgt aggtcttcct cagaaggttg ttcatatcca    120
58 tcttggtacc acactaatct tgcgatcaca tattcttgat ttgcagtcaa aggtggaaca    180
60 tttcgaattc tgttttcagc aagaatcttg tctgacaaaa atttcacttt agttgcttct    240
62 ggaggtaatg ggtcgcattt catgaccgca ggcaaaatat caggcttctg aagtaatgca    300
64 gaattcgcta agggagcagc agattttcca acggtacctg atattggtcc gatgtccttt    360
66 tccttctgtg ccttcttttc ctttcgcttc atggcgcatt ggttttcggg aaccacgcac    420
68 tcggggcgca ttccgacagc caaaca                                          446
71 <210> SEQ ID NO: 3
72 <211> LENGTH: 350
73 <212> TYPE: DNA
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 76 <400> SEQUENCE: 3
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 79 gaaaatctgc tgctccctta gcgaattctg cattccttca gaagcctgat attttgcctg    120
 81 cggtcatgaa atgcgaccca ttacctccag aagcaactaa agtgaaattt ttgtcagaca    180
 83 agattcttgc tgaaaacaga attcgaaatg ttccaccttt gactgcaaat caagaatatg    240
 85 tgatcgcaag attagtgtgg taccaagatg gatatgaaca accttctgag gaagacctac    300
 87 gaaggataat gataagtaca ccaggtgaag atgaagctgt tgaatttcgg                350
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 91 <211> LENGTH: 350
 92 <212> TYPE: DNA
 93 <213> ORGANISM: Ctenocephalides felis
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 96 ccgaaattca acagcttcat cttcacctgg tgtacttatc attatccttc gtaggtcttc     60
 98 ctcagaaggt tgttcatatc catcttggta ccacactaat cttgcgatca catattcttg    120
100 atttgcagtc aaaggtggaa catttcgaat tctgttttca gcaagaatct tgtctgacaa    180
102 aaatttcact ttagttgctt ctggaggtaa tgggtcgcat ttcatgaccg caggcaaaat    240
104 atcaggcttc tgaaggaatg cagaattcgc taagggagca gcagattttc caacggtacc    300
106 tgatattgcc gatgtccttt tccttctgtg ccttcttttc ctttcgcttc               350
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 2822
111 <212> TYPE: DNA
112 <213> ORGANISM: Ctenocephalides felis
114 <220> FEATURE:
115 <221> NAME/KEY: CDS
116 <222> LOCATION: (605)..(2287)
117 <223> OTHER INFORMATION:
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W--> 120 <400> 5
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123 atgtataatt gtatttgtga aatgaaacac atgctaccta aaaactgatt cgtatgccgc    120
125 tctatcaatc agaaatgata attaaacaat ttttttatat tgaaatagaa catattatgt    180
127 tcatatgtca ataacaaatt ttaaacattc atccaagtta cctattttat gcttttaaga    240
129 tattatttat ttatttattt tgttttgtaa aatttaaaat tttacataaa tactttctaa   .300
131 ctatgaatat aaattaatat acaaaagatt ttgaaactaa gaggaaaagt aattataatc    360
133 attttaatca ttaaattata tactcaaaat gatacaatta gattttacag tcacacacat    420
135 taggtacaga gattcaatta tgaattagga gttgagaaat gctttcgagt aaaatctgca    480
137 ataagatgac tatattccta aggatgttat gtcagtcata aataaaaatc actatatttt    540
139 caatttgtgt atggtgatct tctaaaggat aaatgtgtga agtgaaatac cttgcattat    600
141 caac atg aaa cga cgt tgg tct aac aac ggt ggc ttc caa acc ttg cgg     649
142      Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Gln Thr Leu Arg
143       1               5                  10                  15
145 atg ctc gaa gat gtt gca tct ggt gag gta acg tcg tct tct ggt ggc     697
146 Met Leu Glu Asp Val Ala Ser Gly Glu Val Thr Ser Ser Ser Gly Gly
147                 20                  25                  30
149 gcc ctg gct gcg ttg agt ccg gct tcg tta ggt tcg ccc gag aca tat     745
150 Ala Leu Ala Ala Leu Ser Pro Ala Ser Leu Gly Ser Pro Glu Thr Tyr
151             35                  40                  45
153 gcc gag ctg gat ttg tgg gtg tac gag gaa gct ggc tta cat cca ggt     793
154 Ala Glu Leu Asp Leu Trp Val Tyr Glu Glu Ala Gly Leu His Pro Gly
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155        50                  55                  60
157 tca ggt gtg caa gga tgc ggt gcg gtc gcc gcc ttg cca tcg atc gcg      841
158 Ser Gly Val Gln Gly Cys Gly Ala Val Ala Ala Leu Pro Ser Ile Ala
159    65                  70                  75
161 aca cag gtc ccc cta gga ttg ccc gct atg gac cta ccg cac acg cct      889
162 Thr Gln Val Pro Leu Gly Leu Pro Ala Met Asp Leu Pro His Thr Pro
163 80                  85                  90                  95
165 cgg agt gac agt gcg ggt agc atc tca tca gga cga gaa gac ctg tca      937
166 Arg Ser Asp Ser Ala Gly Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser
167               100                 105                 110
169 ccg cct agt tct ttg aac ggc tat tca gca gat ggc tgc gaa gcg aag      985
170 Pro Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asp Gly Cys Glu Ala Lys
171               115                 120                 125
173 aag gcc aag aaa ggg ccg gcg ccg cgg cag cag gag gaa cta tgt ctt     1033
174 Lys Ala Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu
175               130                 135                 140
177 gtg tgc ggc gac cgt gcc tcc gga tat cat tac aac gct ctt act tgt     1081
178 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
179    145                 150                 155
181 gaa gga tgc aaa ggt ttt ttc cga cga agt gtg act aag aat gcc gtg     1129
182 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys.Asn Ala Val
183 160                 165                 170                 175
185 tac gtg tgc aag ttt ggg cac acg tgc gaa atg gac atg tat atg cga     1177
186 Tyr Val Cys Lys Phe Gly His Thr Cys Glu Met Asp Met Tyr Met Arg
187               180                 185                 190
189 cgc aaa tgt cag gaa tgt agg ctc aag aaa tgt ttg gct gtc gga atg     1225
190 Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met
191               195                 200                 205
193 cgc ccc gag tgc gtg gtt ccc gaa aac caa tgc gcc atg aag cga aag     1273
194 Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys
195               210                 215                 220
197 gaa aag aag gca cag aag gaa aag gac atc gga cca ata tca ggt acc     1321
198 Glu Lys Lys Ala Gln Lys Glu Lys Asp Ile Gly Pro Ile Ser Gly Thr
199    225                 230                 235
201 gtt gga aaa tct gct gct ccc tta gcg aat tct gca tta ctt cag aag     1369
202 Val Gly Lys Ser Ala Ala Pro Leu Ala Asn Ser Ala Leu Leu Gln Lys
203 240                 245                 250                 255
205 cct gat att ttg cct gcg gtc atg aaa tgc gac cca tta cct cca gaa     1417
206 Pro Asp Ile Leu Pro Ala Val Met Lys Cys Asp Pro Leu Pro Pro Glu
207               260                 265                 270
209 gca act aaa gtg aaa ttt ttg tca gac aag att ctt gct gaa aac aga     1465
210 Ala Thr Lys Val Lys Phe Leu Ser Asp Lys Ile Leu Ala Glu Asn Arg
211               275                 280                 285
213 att cga aat gtt cca cct ttg act gca aat caa gaa tat gtg atc gca     1513
214 Ile Arg Asn Val Pro Pro Leu Thr Ala Asn Gln Glu Tyr Val Ile Ala
215               290                 295                 300
217 aga tta gtg tgg tac caa gat gga tat gaa caa cct tct gag gaa gac     1561
218 Arg Leu Val Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
219    305                 310                 315
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221 cta cga agg ata atg ata agt aca cca gct gaa gat gaa gct ctt gaa    1609
222 Leu Arg Arg Ile Met Ile Ser Thr Pro Ala Glu Asp Glu Ala Leu Glu
223 320             325             330             335
225 ttt cgg cat ata act gaa att acc ata ctt act gtg cag ctt ata gtg    1657
226 Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val
227             340             345             350
229 gaa ttt gca aag ggt tta cca gct ttt acc aaa ata cca caa gaa gat    1705
230 Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp
231             355             360             365
233 caa ata aca tta tta aag gca tgt tca agt gaa gta atg atg ctg cga    1753
234 Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg
235         370             375             380
237 atg gct cgg cgg tac gat gca gtg tcg gat tca atc tta ttc gcg aat    1801
238 Met Ala Arg Arg Tyr Asp Ala Val Ser Asp Ser Ile Leu Phe Ala Asn
239     385             390             395
241 aat cgt tca tat act cgt gac tcc tat aaa atg gct ggt atg gca gat    1849
242 Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp
243 400             405             410             415
245 aca ata gaa gat cta ttg cat ttt tgt cga cag atg tat act atg act    1897
246 Thr Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Thr Met Thr
247             420             425             430
249 gta gac aat gtg gag tat gca cta ata aca gca att gtg att ttt tca    1945
250 Val Asp Asn Val Glu Tyr Ala Leu Ile Thr Ala Ile Val Ile Phe Ser
251             435             440             445
253 gat cga cct gga ttg gaa caa gca gat ctt gtg gaa caa att caa agt    1993
254 Asp Arg Pro Gly Leu Glu Gln Ala Asp Leu Val Glu Gln Ile Gln Ser
255         450             455             460
257 tat tac atc aaa aca tta aag tgc tac att ttg aat cga cat agt ggt    2041
258 Tyr Tyr Ile Lys Thr Leu Lys Cys Tyr Ile Leu Asn Arg His Ser Gly
259     465             470             475
261 gac cct aag tgt gga ata ttg ttt gcc aaa ctt ctt tct att ctt act    2089
262 Asp Pro Lys Cys Gly Ile Leu Phe Ala Lys Leu Leu Ser Ile Leu Thr
263 480             485             490             495
265 gaa tta cgc acg tta gga aat caa aac tca gaa atg tgt ttt gca ctg    2137
266 Glu Leu Arg Thr Leu Gly Asn Gln Asn Ser Glu Met Cys Phe Ala Leu
267             500             505             510
269 aaa ttg aag aac aga aaa ctt cct aga ttt tta gaa gaa att tgg gat    2185
270 Lys Leu Lys Asn Arg Lys Leu Pro Arg Phe Leu Glu Glu Ile Trp Asp
271             515             520             525
273 gtg aca gat aat gtg cct cct acg ata gac agc atg cat agt gta tcg    2233
274 Val Thr Asp Asn Val Pro Pro Thr Ile Asp Ser Met His Ser Val Ser
275         530             535             540
277 gag aat ttc tat aat aat gaa agt aat ggt acc agt gat tct aca cca    2281
278 Glu Asn Phe Tyr Asn Asn Glu Ser Asn Gly Thr Ser Asp Ser Thr Pro
279     545             550             555
281 atg taa agtgctcaga aaatcaacag ctcttttgca tatttgttta ctgtgtactg    2337
282 Met
283 560
285 gtatggaaaa ttaaggtaac attaaaatat tacataagca ccatgggaaa aggccgttaa    2397
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287 ggcaatattt ttgaataaat aatctattga gacggtacca atggtaaact tggaaaaaat  2457
289 tcttctgttt acatattagg agccaagtta aagaataagt atgaatgatt gttgataaat  2517
291 tgcttgtgta acacttcaat ggccttcaat aaaataatgt ttaacaacgt cgataggaaa  2577
293 ttaaaaagaa atcatgtgta ataaaatcat ttgtaggccg gccatactga tttacctata  2637
295 ttaagcagaa acttcttaat gtataaatat attttttgctt tgcaaggtaa aaccttctca  2697
297 atgcaacaat gaattatata tataaacatt gattattttta tcgttagaat ttgaattttg  2757
299 tgttgtggga gaattgtatt tggattagat aaataggctg tgaaaaataa aaaaaaaaaa  2817
301 aaaaa                                                              2822
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 560
306 <212> TYPE: PRT
307 <213> ORGANISM: Ctenocephalides felis
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316             20                  25                  30
319 Leu Ala Ala Leu Ser Pro Ala Ser Leu Gly Ser Pro Glu Thr Tyr Ala
320          35                  40                  45
323 Glu Leu Asp Leu Trp Val Tyr Glu Glu Ala Gly Leu His Pro Gly Ser
324      50                  55                  60
327 Gly Val Gln Gly Cys Gly Ala Val Ala Ala Leu Pro Ser Ile Ala Thr
328 65                  70                  75                  80
331 Gln Val Pro Leu Gly Leu Pro Ala Met Asp Leu Pro His Thr Pro Arg
332             85                  90                  95
335 Ser Asp Ser Ala Gly Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser Pro
336             100                 105                 110
339 Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asp Gly Cys Glu Ala Lys Lys
340         115                 120                 125
343 Ala Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu Val
344     130                 135                 140
347 Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu
348 145                 150                 155                 160
351 Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr
352             165                 170                 175
355 Val Cys Lys Phe Gly His Thr Cys Glu Met Asp Met Tyr Met Arg Arg
356             180                 185                 190
359 Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg
360         195                 200                 205
363 Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys Glu
364     210                 215                 220
367 Lys Lys Ala Gln Lys Glu Lys Asp Ile Gly Pro Ile Ser Gly Thr Val
368 225                 230                 235                 240
371 Gly Lys Ser Ala Ala Pro Leu Ala Asn Ser Ala Leu Leu Gln Lys Pro
372             245                 250                 255
375 Asp Ile Leu Pro Ala Val Met Lys Cys Asp Pro Leu Pro Pro Glu Ala
376             260                 265                 270
379 Thr Lys Val Lys Phe Leu Ser Asp Lys Ile Leu Ala Glu Asn Arg Ile
380         275                 280                 285
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 15
Seq#:51; N Pos. 10

VERIFICATION SUMMARY
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:120 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:117
L:565 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:562
L:990 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:987
L:1527 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:1524
L:2229 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:2226
L:2556 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2553
L:2853 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:2850
L:3206 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:3203
L:3739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:3817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
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